Association of novel single nucleotide polymorphisms of the \textit{CXCR1} gene with the milk performance traits of Chinese native cattle

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ABSTRACT. Mastitis is an economically devastating disease affecting the dairy industry. Dairy cows with mastitis give reduced milk yield and produce milk that is unfit for consumption. The chemokine receptor CXCR1 is an excellent prospective genetic marker for mastitis resistance in cattle because it regulates neutrophil migration, killing, and survival during infection. We detected 4 single nucleotide polymorphisms (SNPs) of the \textit{CXCR1} gene in Chinese native cattle and analyzed their associations with milk traits. Screening for genetic variations in \textit{CXCR1} among 648 Chinese Holstein, Luxi Yellow, and Bohai Black cattle by created restriction site polymerase chain reaction (PCR), nested PCR, and DNA sequencing revealed 4 new SNPs with allelic frequencies ranging from 0.676 to 0.821, 0.706 to 0.803, 0.647 to 0.824, and 0.558 to 0.581. All four \textit{CXCR1} gene SNPs were located in exon II. Two SNPs, c.337A>G and c.365C>T, were nonsynonymous mutations [ATC (Ile) > GTC (Val) and GCC (Ala) > GTC (Val)], whereas two, c.291C>T and c.333C>T, were synonymous mutations [TTC (Gly) > TTT (Gly) and GGC (Phe) > GGT (Phe)]. Statistical analyses revealed
the significant association of c.337A>G and c.365C>T with the somatic cell score, which suggests the possible role of these SNPs in the host response against mastitis. Our data suggest that combined genotypes CCAC/CCGC, CCAC/CTAT, and CCAT/CTAT (lowest somatic cell scores); CTAC/CTAT (highest protein rate); CCAC/CTGC (highest fat rate); and CCAT/CTAT (highest 305-day milk yield) can be used as possible candidates for marker-assisted selection in dairy cattle breeding programs.

**Key words:** Chinese native cattle; CXCR1; SNPs; Milk traits; SCS